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RAW SEQUENCE LISTING

DATE: 05/02/2001

PATENT APPLICATION: US/09/835,684

TIME: 12:12:30

Input Set : A:\E72011.app

Output Set: N:\CRF3\05022001\I835684.raw

ENTERED

2

3 <110> APPLICANT: Wei, Zhong-Min
 4 Qiu, Dewen
 5 Remick, Dean
 7 <120> TITLE OF INVENTION: TREATMENT OF FRUITS OR VEGETABLES WITH HYPERSENSITIVE
 8 RESPONSE ELICITOR TO CONTROL POSTHARVEST DISEASE OR
 9 DESICCATION
 11 <130> FILE REFERENCE: 21829/71
~~C--> 13 <140> CURRENT APPLICATION NUMBER: US/09/835,684~~
 C--> 14 <141> CURRENT FILING DATE: 2001-04-16
 16 <150> PRIOR APPLICATION NUMBER: 60/198,359
 17 <151> PRIOR FILING DATE: 2000-04-19
 19 <160> NUMBER OF SEQ ID NOS: 12
 21 <170> SOFTWARE: PatentIn Ver. 2.1
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 338
 25 <212> TYPE: PRT
 26 <213> ORGANISM: Erwinia chrysanthemi
 28 <400> SEQUENCE: 1
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 30 1 5 10 15
 32 Gly Leu Gly Ala Gln Gly Leu Lys Gly Leu Asn Ser Ala Ala Ser Ser
 33 20 25 30
 35 Leu Gly Ser Ser Val Asp Lys Leu Ser Ser Thr Ile Asp Lys Leu Thr
 36 35 40 45
 38 Ser Ala Leu Thr Ser Met Met Phe Gly Gly Ala Leu Ala Gln Gly Leu
 39 50 55 60
 41 Gly Ala Ser Ser Lys Gly Leu Gly Met Ser Asn Gln Leu Gly Gln Ser
 42 65 70 75 80
 44 Phe Gly Asn Gly Ala Gln Gly Ala Ser Asn Leu Leu Ser Val Pro Lys
 45 85 90 95
 47 Ser Gly Gly Asp Ala Leu Ser Lys Met Phe Asp Lys Ala Leu Asp Asp
 48 100 105 110
 50 Leu Leu Gly His Asp Thr Val Thr Lys Leu Thr Asn Gln Ser Asn Gln
 51 115 120 125
 53 Leu Ala Asn Ser Met Leu Asn Ala Ser Gln Met Thr Gln Gly Asn Met
 54 130 135 140
 56 Asn Ala Phe Gly Ser Gly Val Asn Asn Ala Leu Ser Ser Ile Leu Gly
 57 145 150 155 160
 59 Asn Gly Leu Gly Gln Ser Met Ser Gly Phe Ser Gln Pro Ser Leu Gly
 60 165 170 175
 62 Ala Gly Gly Leu Gln Gly Leu Ser Gly Ala Gly Ala Phe Asn Gln Leu
 63 180 185 190
 65 Gly Asn Ala Ile Gly Met Gly Val Gly Gln Asn Ala Ala Leu Ser Ala
 66 195 200 205
 68 Leu Ser Asn Val Ser Thr His Val Asp Gly Asn Asn Arg His Phe Val
 69 210 215 220
 71 Asp Lys Glu Asp Arg Gly Met Ala Lys Glu Ile Gly Gln Phe Met Asp

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72 225          230          235          240
74 Gln Tyr Pro Glu Ile Phe Gly Lys Pro Glu Tyr Gln Lys Asp Gly Trp
75          245          250          255
77 Ser Ser Pro Lys Thr Asp Asp Lys Ser Trp Ala Lys Ala Leu Ser Lys
78          260          265          270
80 Pro Asp Asp Asp Gly Met Thr Gly Ala Ser Met Asp Lys Phe Arg Gln
81          275          280          285
83 Ala Met Gly Met Ile Lys Ser Ala Val Ala Gly Asp Thr Gly Asn Thr
84          290          295          300
86 Asn Leu Asn Leu Arg Gly Ala Gly Gly Ala Ser Leu Gly Ile Asp Ala
87 305          310          315          320
89 Ala Val Val Gly Asp Lys Ile Ala Asn Met Ser Leu Gly Lys Leu Ala
90          325          330          335
92 Asn Ala
96 <210> SEQ ID NO: 2
97 <211> LENGTH: 2141
98 <212> TYPE: DNA
99 <213> ORGANISM: Erwinia chrysanthemi
101 <400> SEQUENCE: 2
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103 gcgttttatgg ccgcgatgaa ccggcatcag gcggcgcgct ggtcgccgca atccggcgctc 120
104 gatctgggtat ttacgttttgg ggacaccggg cgtgaactca tgatgcagat tcagccggggg 180
105 cagcaatatac ccggcatgtt gcgcacgctg ctgcctcgtc gttatcagca ggcggcagag 240
106 tgcgatggct gccatctgtg cctgaacggc agcgatgtat tgatcctctg gtggccgctg 300
107 ccgtcggatc ccggcagtta tccgcaggtg atcgaacgtt tgtttgaact ggcgggaatg 360
108 acgttgccgt cgctatccat agcacgcagc gcgcgtccgc agacagggaa cggacgcgcc 420
109 cgatcattaa gataaaggcg gcttttttta ttgcaaacg gtaacggtga ggaaccgttt 480
110 caccgtcggc gtcactcagt aacaagtatc catcatgatg cctacatcgg gatcggcgctg 540
111 ggcattccgtt gcagatactt ttgcgaacac ctgacatgaa tgaggaaacg aaattatgca 600
112 aattacgatac aaagcgcaca tcggcggtga tttggcgctc tccggtctgg ggctgggtgc 660
113 tcagggactg aaaggactga attccgcggc ttcatcgtg ggttcacgagc tggataaact 720
114 gagcagcacc atcgataagt tgacctccgc gctgacttgc atgatgtttg gcggcgcgct 780
115 ggcgcagggg ctgggcgcca gctgaaggg gctggggatg agcaatcaac tgggccagtc 840
116 tttcggcaat ggcgcgcagg gtgcgagcaa cctgctatcc gtaccgaaat ccggcggcga 900
117 tgcgttgtca aaaatgtttg ataaagcgct ggacgatctg ctgggtcatg acaccgtgac 960
118 caagctgact aaccagagca accaactggc taattcaatg ctgaacgcca gccagatgac 1020
119 ccagggtaat atgaatgcgt tcggcagcgg tgtgaacaac gcaactgctg ccattctcgg 1080
120 caacggtctc ggccagtcga tgagtggctt ctctcagcct tctctggggg caggcggtt 1140
121 gcagggcctg agcggcgcgg gtgcattcaa ccagttgggt aatgccatcg gcatggcgct 1200
122 ggggcagaat gctgcgctga gtgcgttgag taacgtcagc acccacgtag acggttaaca 1260
123 ccgccacttt gtagataaag aagatcgcgg catggcgaaa gagatcggcc agtttatgga 1320
124 tcagtatccg gaaatattcg gtaaaccgga ataccagaaa gatggctgga gttcgccgaa 1380
125 gacggacgac aaatcctggg ctaaagcgct gagtaaaccg gatgatgacg gtatgaccgg 1440
126 cgccagcatg gacaaattcc gtcaggcgat ggggtatgatc aaaagcgcgg tggcggtgta 1500
127 taccggcaat accaacctga acctgcgtgg cgcgggcggt gcatcgtggt gtatcgatgc 1560
128 ggctgtcgtc ggcgataaaa tagccaacat gtcgctgggt aagctggcca acgcctgata 1620
129 atctgtgctg gcctgataaa gcggaaacga aaaaagagac ggggaagcct gtctcttttc 1680
130 ttattatgcg gtttatgcgg ttacctggac cggttaatca tcgtcatcga tctggtacaa 1740
131 acgcacattt tcccgttcat tcgcgtcgtt acgcgccaca atcgcgatgg catcttcctc 1800

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132 gtcgctcaga ttgcgcggct gatggggaac gccgggtgga atatagagaa actcgccggc 1860
133 cagatggaga cacgtctgcg ataaatctgt gccgtaacgt gtttctatcc gcccttttag 1920
134 cagatagatt gcggtttcgt aatcaacatg gtaatgcggt tccgcctgtg cgccggccgg 1980
135 gatcaccaca atattcatag aaagctgtct tgcacctacc gtatcgcggt agataccgac 2040
136 aaaatagggc agtttttgcg tggatatcgt ggggtgttcc ggcctgacaa tcttgagttg 2100
137 gttcgtcatc atctttctcc atctgggcga cctgatcggt t 2141

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140 <210> SEQ ID NO: 3

141 <211> LENGTH: 403

142 <212> TYPE: PRT

143 <213> ORGANISM: Erwinia amylovora

145 <400> SEQUENCE: 3

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146 Met Ser Leu Asn Thr Ser Gly Leu Gly Ala Ser Thr Met Gln Ile Ser
147 1 5 10 15
149 Ile Gly Gly Ala Gly Gly Asn Asn Gly Leu Leu Gly Thr Ser Arg Gln
150 20 25 30
152 Asn Ala Gly Leu Gly Gly Asn Ser Ala Leu Gly Leu Gly Gly Asn
153 35 40 45
155 Gln Asn Asp Thr Val Asn Gln Leu Ala Gly Leu Leu Thr Gly Met Met
156 50 55 60
158 Met Met Met Ser Met Met Gly Gly Gly Gly Leu Met Gly Gly Gly Leu
159 65 70 75 80
161 Gly Gly Gly Leu Gly Asn Gly Leu Gly Gly Ser Gly Gly Leu Gly Glu
162 85 90 95
164 Gly Leu Ser Asn Ala Leu Asn Asp Met Leu Gly Gly Ser Leu Asn Thr
165 100 105 110
167 Leu Gly Ser Lys Gly Gly Asn Asn Thr Thr Ser Thr Thr Asn Ser Pro
168 115 120 125
170 Leu Asp Gln Ala Leu Gly Ile Asn Ser Thr Ser Gln Asn Asp Asp Ser
171 130 135 140
173 Thr Ser Gly Thr Asp Ser Thr Ser Asp Ser Ser Asp Pro Met Gln Gln
174 145 150 155 160
176 Leu Leu Lys Met Phe Ser Glu Ile Met Gln Ser Leu Phe Gly Asp Gly
177 165 170 175
179 Gln Asp Gly Thr Gln Gly Ser Ser Ser Gly Gly Lys Gln Pro Thr Glu
180 180 185 190
182 Gly Glu Gln Asn Ala Tyr Lys Lys Gly Val Thr Asp Ala Leu Ser Gly
183 195 200 205
185 Leu Met Gly Asn Gly Leu Ser Gln Leu Leu Gly Asn Gly Gly Leu Gly
186 210 215 220
188 Gly Gly Gln Gly Gly Asn Ala Gly Thr Gly Leu Asp Gly Ser Ser Leu
189 225 230 235 240
191 Gly Gly Lys Gly Leu Gln Asn Leu Ser Gly Pro Val Asp Tyr Gln Gln
192 245 250 255
194 Leu Gly Asn Ala Val Gly Thr Gly Ile Gly Met Lys Ala Gly Ile Gln
195 260 265 270
197 Ala Leu Asn Asp Ile Gly Thr His Arg His Ser Ser Thr Arg Ser Phe
198 275 280 285
200 Val Asn Lys Gly Asp Arg Ala Met Ala Lys Glu Ile Gly Gln Phe Met
201 290 295 300

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203 Asp Gln Tyr Pro Glu Val Phe Gly Lys Pro Gln Tyr Gln Lys Gly Pro
204 305                      310                      315                      320
206 Gly Gln Glu Val Lys Thr Asp Asp Lys Ser Trp Ala Lys Ala Leu Ser
207                      325                      330                      335
209 Lys Pro Asp Asp Asp Gly Met Thr Pro Ala Ser Met Glu Gln Phe Asn
210                      340                      345                      350
212 Lys Ala Lys Gly Met Ile Lys Arg Pro Met Ala Gly Asp Thr Gly Asn
213                      355                      360                      365
215 Gly Asn Leu Gln Ala Arg Gly Ala Gly Gly Ser Ser Leu Gly Ile Asp
216                      370                      375                      380
218 Ala Met Met Ala Gly Asp Ala Ile Asn Asn Met Ala Leu Gly Lys Leu
219 385                      390                      395                      400

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221 Gly Ala Ala

225 <210> SEQ ID NO: 4

226 <211> LENGTH: 1288

227 <212> TYPE: DNA

228 <213> ORGANISM: Erwinia amylovora

230 <400> SEQUENCE: 4

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231 aagcttcggc atggcacgtt tgaccgttgg gtcggcaggg tacgtttgaa ttattcataa 60
232 gaggaatacg ttatgagtct gaatacaagt gggctgggag cgtcaacgat gcaaatttct 120
233 atcggcgggtg cggggcgaaa taacgggttg ctgggtacca gtcgccagaa tgctgggttg 180
234 ggtggcaatt ctgcaactggg gctgggcggc ggtaatcaaa atgataccgt caatcagctg 240
235 gctggcttac tcaccggcat gatgatgatg atgagcatga tgggcgggtg tgggctgatg 300
236 ggcggtggtc taggcggtgg cttaggtaat ggcttgggtg gctcaggtg cctgggcgaa 360
237 ggactgtcga acgcgctgaa cgatatgtta ggcggttcgc tgaacacgct gggctcgaaa 420
238 ggcggcaaca ataccacttc aacaacaaat tccccgctgg accaggcgct gggatttaac 480
239 tcaacgtccc aaaacgacga ttccacctcc ggcacagatt ccacctcaga ctccagcgac 540
240 ccgatgcagc agctgctgaa gatgttcagc gagataatgc aaagcctggt tggatgatgg 600
241 caagatggca cccagggcag ttcctctggg ggcaagcagc cgaccgaagg cgagcagaac 660
242 gcctataaaa aaggagtcac tgatgcgctg tcgggcctga tgggtaatgg tctgagccag 720
243 ctcccttgga acgggggact gggaggtggt cagggcggtg atgctggcac gggctctgac 780
244 ggttcgctgc tgggcggcaa agggctgcaa aacctgagcg ggccggtgga ctaccagcag 840
245 ttaggtaacg ccgtgggtac cggtatcggg atgaaagcgg gcattcaggc gctgaatgat 900
246 atcggtacgc acaggcacag ttcaaccctg tctttcgtca ataaaggcga tcgggcgatg 960
247 gcgaaggaaa tcggtcagtt catggaccag tatcctgagg tgtttgcaa gccgcagtac 1020
248 cagaaaggcc cgggtcagga ggtgaaaacc gatgacaaat catgggcaaa agcactgagc 1080
249 aagccagatg acgacggaat gacaccagcc agtatggagc agttcaacaa agccaagggc 1140
250 atgatcaaaa ggcccatggc gggtgatacc ggcaacggca acctgcaggc acgcggtgcc 1200
251 ggtggttctt cgctgggtat tgatgccatg atggccggtg atgccattaa caatatggca 1260
252 cttggcaagc tgggcgcggc ttaagctt

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1288

255 <210> SEQ ID NO: 5

256 <211> LENGTH: 447

257 <212> TYPE: PRT

258 <213> ORGANISM: Erwinia amylovora

260 <400> SEQUENCE: 5

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262 1                      5                      10                      15
264 Phe Gln Ser Gly Gly Asp Asn Gly Leu Gly Gly His Asn Ala Asn Ser
265                      20                      25                      30

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267 Ala Leu Gly Gln Gln Pro Ile Asp Arg Gln Thr Ile Glu Gln Met Ala
268      35      40      45
270 Gln Leu Leu Ala Glu Leu Leu Lys Ser Leu Leu Ser Pro Gln Ser Gly
271      50      55      60
273 Asn Ala Ala Thr Gly Ala Gly Gly Asn Asp Gln Thr Thr Gly Val Gly
274      65      70      75      80
276 Asn Ala Gly Gly Leu Asn Gly Arg Lys Gly Thr Ala Gly Thr Thr Pro
277      85      90      95
279 Gln Ser Asp Ser Gln Asn Met Leu Ser Glu Met Gly Asn Asn Gly Leu
280      100      105      110
282 Asp Gln Ala Ile Thr Pro Asp Gly Gln Gly Gly Gly Gln Ile Gly Asp
283      115      120      125
285 Asn Pro Leu Leu Lys Ala Met Leu Lys Leu Ile Ala Arg Met Met Asp
286      130      135      140
288 Gly Gln Ser Asp Gln Phe Gly Gln Pro Gly Thr Gly Asn Asn Ser Ala
289      145      150      155      160
291 Ser Ser Gly Thr Ser Ser Ser Gly Gly Ser Pro Phe Asn Asp Leu Ser
292      165      170      175
294 Gly Gly Lys Ala Pro Ser Gly Asn Ser Pro Ser Gly Asn Tyr Ser Pro
295      180      185      190
297 Val Ser Thr Phe Ser Pro Pro Ser Thr Pro Thr Ser Pro Thr Ser Pro
298      195      200      205
300 Leu Asp Phe Pro Ser Ser Pro Thr Lys Ala Ala Gly Gly Ser Thr Pro
301      210      215      220
303 Val Thr Asp His Pro Asp Pro Val Gly Ser Ala Gly Ile Gly Ala Gly
304      225      230      235      240
306 Asn Ser Val Ala Phe Thr Ser Ala Gly Ala Asn Gln Thr Val Leu His
307      245      250      255
309 Asp Thr Ile Thr Val Lys Ala Gly Gln Val Phe Asp Gly Lys Gly Gln
310      260      265      270
312 Thr Phe Thr Ala Gly Ser Glu Leu Gly Asp Gly Gly Gln Ser Glu Asn
313      275      280      285
315 Gln Lys Pro Leu Phe Ile Leu Glu Asp Gly Ala Ser Leu Lys Asn Val
316      290      295      300
318 Thr Met Gly Asp Asp Gly Ala Asp Gly Ile His Leu Tyr Gly Asp Ala
319      305      310      315      320
321 Lys Ile Asp Asn Leu His Val Thr Asn Val Gly Glu Asp Ala Ile Thr
322      325      330      335
324 Val Lys Pro Asn Ser Ala Gly Lys Lys Ser His Val Glu Ile Thr Asn
325      340      345      350
327 Ser Ser Phe Glu His Ala Ser Asp Lys Ile Leu Gln Leu Asn Ala Asp
328      355      360      365
330 Thr Asn Leu Ser Val Asp Asn Val Lys Ala Lys Asp Phe Gly Thr Phe
331      370      375      380
333 Val Arg Thr Asn Gly Gly Gln Gln Gly Asn Trp Asp Leu Asn Leu Ser
334      385      390      395      400
336 His Ile Ser Ala Glu Asp Gly Lys Phe Ser Phe Val Lys Ser Asp Ser
337      405      410      415
339 Glu Gly Leu Asn Val Asn Thr Ser Asp Ile Ser Leu Gly Asp Val Glu

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VERIFICATION SUMMARY

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DATE: 05/02/2001

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L:13 M:270 C: Current Application Number differs, Replaced Application Number

L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date